

SEQUENCE LISTING



#5

1636

9/338,063

(1) GENERAL INFORMATION:

- 10640
- (i) APPLICANT: GOTO, Masaaki  
TSUDA, Eisuke  
MOCHIZUKI, Shin'ichi  
YANO, Kazuki  
KOBAYASHI, Fumie  
SHIMA, Nobuyuki  
YASUDA, Hisataka  
NAKAGAWA, Nobuaki  
MORINAGA, Tomonori  
UEDA, Masatsugu  
HIGASHIO, Kanji
- (ii) TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
- (iii) NUMBER OF SEQUENCES: 108
- (iv) CORRESPONDENCE ADDRESS:  
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(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/338,063  
(B) FILING DATE: 23-JUN-1999  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: JP 54977/1995  
(B) FILING DATE: 20-FEB-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: JP 207508/1995  
(B) FILING DATE: 21-JUL-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/JP96/00374  
(B) FILING DATE: 20-FEB-1996
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/915,004  
(B) FILING DATE: 20-AUG-1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: MOORE, Ronda P.  
(B) REGISTRATION NUMBER: 44,244  
(C) REFERENCE/DOCKET NUMBER: FJN-060DV2
- (ix) TELECOMMUNICATION INFORMATION:  
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- 64

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B

(ix) FEATURE:  
    (A) NAME/KEY: Peptide  
    (B) LOCATION: 1..6  
    (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Tyr His Phe Pro Lys  
1                    5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
    (A) NAME/KEY: Peptide  
    (B) LOCATION: 1..14  
    (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 12 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
    (A) NAME/KEY: Peptide  
    (B) LOCATION: 1..12  
    (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 380 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
    (A) NAME/KEY: Protein  
    (B) LOCATION: 1..380  
    (D) OTHER INFORMATION: /note= "(OCIF protein without signal peptide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His  
1 5 10 15  
Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His  
20 25 30  
Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr  
35 40 45  
Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro  
50 55 60  
Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His  
65 70 75 80  
Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe  
85 90 95  
Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala  
100 105 110  
Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe  
115 120 125  
Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn  
130 135 140  
Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His  
145 150 155 160  
Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile  
165 170 175  
Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
180 185 190  
Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly  
195 200 205  
Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser  
210 215 220  
Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
225 230 235 240  
Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys  
245 250 255  
Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu  
260 265 270  
Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala  
275 280 285  
Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile  
290 295 300  
Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
305 310 315 320  
Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe  
325 330 335  
Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His  
340 345 350  
Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
355 360 365  
Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

66

B

(A) LENGTH: 401 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1..380  
(D) OTHER INFORMATION: /note= "(OCIF protein)"

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0  
(D) OTHER INFORMATION: /note= "(signal peptide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15						-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
	30						35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
	45					50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70					75		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
			80						85					90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
		95						100					105			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
	110						115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	
			160						165					170		
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	
		175						180					185			
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	
	190						195					200				
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	
	205					210					215					
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	
220					225					230					235	
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	
			240						245					250		
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	
		255						260					265			
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	
		270					275					280				

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAAG	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTTCTACAA	AGTTTACGCC	TAAGTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080

GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140  
TATCAGAAGT TATTTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200  
TTATAA 1206

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..15  
(D) OTHER INFORMATION: /note= "(a N-terminal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1185  
(D) OTHER INFORMATION: /note= "(OCIF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAACAACCT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCCGTGTG CAAGGAGTGC AATCGCACCC ACAACCGCGT GTGCGAATGC 300  
AAGGAAGGGC GCTACCTTGA GATAGAGTTC TGCTTGAAAC ATAGGAGCTG CCCTCCTGGA 360  
TTTGGAGTGG TGCAAGCTGG AACCACAGAG CGAAATACAG TTTGCAAAAG ATGTCCAGAT 420  
GGGTCTCTCT CAAATGAGAC GTCATCTAAA GCACCCTGTA GAAAACACAC AAATTGCAGT 480  
GTCTTTGGTC TCCTGCTAAC TCAGAAAGGA AATGCAACAC ACGACAACAT ATGTTCCGGA 540  
AACAGTGAAT CAACTCAAAA ATGTGGAATA GATGTTACCC TGTGTGAGGA GGCATTCTTC 600  
AGGTTTGCTG TTCCTACAAA GTTTACGCCT AACTGGCTTA GTGTCTTGGT AGACAATTTG 660  
CCTGGCACCA AAGTAAACGC AGAGAGTGTA GAGAGGATAA AACGGCAACA CAGCTCACAA 720  
GAACAGACTT TCCAGCTGCT GAAGTTATGG AAACATCAAA ACAAAGACCA AGATATAGTC 780  
AAGAAGATCA TCCAAGATAT TGACCTCTGT GAAAACAGCG TGCAGCGGCA CATTGGACAT 840  
GCTAACCTCA CCTTCGAGCA GCTTCGTAGC TTGATGGAAA GCTTACCGGG AAAGAAAGTG 900

GGAGCAGAAG ACATTGAAAA AACAAATAAAG GCATGCAAAC CCAGTGACCA GATCCTGAAG 960  
 CTGCTCAGTT TGTGGCGAAT AAAAAATGGC GACCAAGACA CCTTGAAGGG CCTAATGCAC 1020  
 GCACTAAAGC ACTCAAAGAC GTACCACTTT CCCAAAACCTG TCACTCAGAG TCTAAAGAAG 1080  
 ACCATCAGGT TCCTTCACAG CTTCACAATG TACAAATTGT ATCAGAAGTT ATTTTTAGAA 1140  
 ATGATAGGTA ACCAGGTCCA ATCAGTAAAA ATAAGCTGCT TATAA 1185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: /note= "(OCIF2)"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile		
-20					-15						-10						
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp		
-5				1				5					10				
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr		
			15					20					25				
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro		
		30					35					40					
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys		
	45					50					55						
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg		
60					65					70					75		
Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu		
			80					85						90			
Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr		
			95					100					105				
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser		
		110					115					120					
Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser		
	125					130					135						
Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn		
140					145					150					155		
Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val		
			160						165					170			
Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe		
		175						180					185				
Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys		
		190					195					200					
Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln		

205	210	215
Glu Gln Thr Phe Gln Leu Lys Leu Trp Lys His Gln Asn Lys Asp 220 225 230 235		
Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn 240 245 250		
Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu 255 260 265		
Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp 270 275 280		
Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys 285 290 295		
Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys 300 305 310 315		
Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys 320 325 330		
Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe 335 340 345		
Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn 350 355 360		
Gln Val Gln Ser Val Lys Ile Ser Cys Leu 365 370		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1089
- (D) OTHER INFORMATION: /note= "(OCIF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAACAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780



AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840  
 GTGCAGCGGC ACATTGGACA TGCTAACCTC AGTTTGTGGC GAATAAAAAA TGGCGACCA 900  
 GACACCTTGA AGGGCCTAAT GCACGCACTA AAGCACTCAA AGACGTACCA CTTTCCCAAA 960  
 ACTGTCCTC AGAGTCTAAA GAAGACCATC AGGTTCTTC ACAGCTTCAC AATGTACAAA 1020  
 TTGTATCAGA AGTTATTTTT AGAAATGATA GGTAACCAGG TCCAATCAGT AAAAATAAGC 1080  
 TGCTTATAA 1089

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: /note= "(OCIF3)"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120  
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135  
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys  
 270 275 280  
 Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys  
 285 290 295  
 Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe  
 300 305 310 315  
 Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn  
 320 325 330  
 Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
 335 340

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 465 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..465  
 (D) OTHER INFORMATION: /note= "(OCIF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAACAAGT TGCTGTGCTG CTCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GTACGTGTCA ATGTGCAGCA	420
AAATTAATTA GGATCATGCA AAGTCAGATA GTTGTGACAG TTTAG	465

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..133  
 (D) OTHER INFORMATION: /note= "(OCIF4)"

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Asn Lys Leu Leu Cys Cys Ser Leu Val Phe Leu Asp Ile Ser Ile
-20                               -15                -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5                               1                     5                10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15                               20                25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30                               35                40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45                               50                55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60                               65                70                75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
80                               85                90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
95                               100               105

Gly Val Val Gln Ala Gly Thr Cys Gln Cys Ala Ala Lys Leu Ile Arg
110                              115                120

Ile Met Gln Ser Gln Ile Val Val Thr Val
125                              130

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 438 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..438  
 (D) OTHER INFORMATION: /note= "(OCIF5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

ATGAACAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG      120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC      180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT      240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC      300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA      360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GATGCAGGAG AAGACCCAAG      420
CCACAGATAT GTATCTGA                                     438

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 amino acids

11 74

b

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1..124  
(D) OTHER INFORMATION: /note= "(OCIF5)"

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10  
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10  
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25  
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40  
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55  
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75  
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90  
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105  
Gly Val Val Gln Ala Gly Cys Arg Arg Arg Pro Lys Pro Gln Ile Cys  
110 115 120  
Ile

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer T3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTAACCCT CACTAAAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..22  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer T7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..20  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACATCAAAAC AAAGACCAAG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..20  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTTGGTCTT TGTTTTGATG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..20  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTATTCGCCA CAAACTGAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGTGAAGCT GTGAAGGAAC

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTCAGTTTG TGGCGAATAA

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGGAGCAG AAGACATTGA

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATGAACAAC TTGCTGTGCT

20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..20  
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF8)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGACAAATGT CCTCCTGGTA

20

- (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..20  
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF9)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGTAGGTAC CAGGAGGACA

20

- (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..20  
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF10)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCTGCCCT CCTGGATTG

20

- (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..20  
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF11)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAACGTAT TTCGCTCTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
IF12)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGTGAGGAG GCATTCTTCA

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..32  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C19SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATCAACTC AAAAAAGTGG AATAGATGTT AC

32

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..32  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C19SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTAACATCTA TTCCACTTTT TTGAGTTGAT TC

32

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:



(A) NAME/KEY: -  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C20SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATAGATGTTA CCCTGAGTGA GGAGGCATTC

30

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C20SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATGCCTCC TCACTCAGGG TAACATCTAT

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C21SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAAGATATTG ACCTCAGTGA AACAGCGTG C

31

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C21SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCACGCTGTT TCACTGAGG GCAATATCTT G

31

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..31  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C22SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:  
AAAACAATAA AGGCAAGCAA ACCCAGTGAC C

31

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..31  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C22SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:  
GGTCACTGGG TTTGCTTGCC TTTATTGTTT T

31

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..31  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C23SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:  
TCAGTAAAAA TAAGCAGCTT ATAAGTGGCC A

31

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..31  
    (D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C23SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGGCCAGTTA TAAGCTGCTT ATTTTACTG A

31

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
 (B) LOCATION: 1..22  
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer  
IF14)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTGGGGTTTA TTGAGGAGA TG

22

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
 (B) LOCATION: 1..36  
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DCR1F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCAGG AACCTTGCCC TGACCACTAC TACACA

36

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
 (B) LOCATION: 1..36  
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DCR1R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCAGGGCAA GGTTCCTGGG TGGTCCAATT AATGGA

36

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DCR2F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCGTGTGCG CCGAATGCAA GGAAGGGCGC TACCTT

36

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DCR2R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTCCTTGCAT TCGGCGCACA CGGTCTTCCA CTTTGC

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DCR3F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACCGCGTGT GCAGATGTCC AGATGGGTTC TTCTCA

36

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DCR3R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTGGACAT CTGCACACGC GGTTGTGGGT GCGATT

36

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR4F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAGTTTGCA AATCCGAAA CAGTGAATCA ACTCAA

36

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR4R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTGTTTCCG GATTTGCAA CTGTATTTCTG CTCTGG

36

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD1F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AATGTGGAAT AGATATTGAC CTCTGTGAAA ACAGCG

36

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD1R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGAGGTCAAT ATCTATTCCA CATTTTTGAG TTGATT

36

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DDD2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGATCATCCA AGACGCACTA AAGCACTCAA AGACGT

36

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
DDD2R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCTTTAGTGC GTCTTGATG ATCTTCTTGA CTATAT

36

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer XhoI  
F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCTCGAGCG CCCAGCCGCC GCCTCCAAG

29

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
IF16)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTGAGTGCT TTAGTGCGTG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CL  
F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TCAGTAAAA TAAGCTAACT GGAAATGGCC

30

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CL  
R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCCATTTCC AGTTAGCTTA TTTTACTGA

30

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CC  
R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGATCCTC AGTGCTTTAG TCGTGCAT

29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD2

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGGATCCTC ATTGGATGAT CTTCTTGAC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD1

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCGGATCCTC ATATTCCACA TTTTGTAGT

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR4

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGGATCCTC ATTTGCAAAC TGTATTTTCG

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR3

R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

87<sub>24</sub>

B



## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C19S"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20          -15          -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5          1          5          10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15          20          25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30          35          40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45          50          55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60          65          70          75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
80          85          90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
95          100          105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
110          115          120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
125          130          135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
140          145          150          155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
160          165          170

Gln Lys Ser Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
175          180          185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
190          195          200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
205          210          215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
220          225          230          235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
240          245          250

```

b

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 401 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..380
  - (D) OTHER INFORMATION: /note= "OCIF-C20S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135  
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Ser Glu Glu Ala Phe Phe Arg  
 175 180 185  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C21S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120  
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135  
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Ser Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 401 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..380  
 (D) OTHER INFORMATION: /note= "OCIF-C22S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	-20	-15	-10	
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	-5	1	5	10
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	15	20	25	
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	30	35	40	
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	45	50	55	
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	60	65	70	75
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	80	85	90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	95	100	105	
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	110	115	120	
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	125	130	135	
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	140	145	150	155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	160	165	170	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	175	180	185	
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	190	195	200	
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	205	210	215	
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	220	225	230	235
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	240	245	250	
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	255	260	265	
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	270	275	280	

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Ser Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C23S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120  
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135  
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Ser  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: /note= "OCIF-DCR1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser  
 -5 1 5 10  
 Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu  
 15 20 25

Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys  
 30 35 40  
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His  
 45 50 55  
 Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu  
 60 65 70 75  
 Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu  
 80 85 90  
 Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe  
 95 100 105  
 Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys  
 110 115 120  
 Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu  
 125 130 135  
 Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro  
 140 145 150 155  
 Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn  
 160 165 170  
 Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln  
 175 180 185  
 Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp  
 190 195 200  
 Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val  
 205 210 215  
 Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser  
 220 225 230 235  
 Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu  
 240 245 250  
 Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu  
 255 260 265  
 Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu  
 270 275 280  
 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val  
 285 290 295  
 Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met  
 300 305 310 315  
 Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val  
 320 325 330  
 Gln Ser Val Lys Ile Ser Cys Leu  
 335

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

b







270 275 280

Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro  
 285 290 295

Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser  
 300 305 310 315

Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly  
 320 325 330

Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
 335 340

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..338  
 (D) OTHER INFORMATION: /note= "OCIF-DCR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Ser  
 110 115 120

Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys  
 125 130 135

Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn  
 140 145 150 155

Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala  
 160 165 170

Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr  
 175 180 185

Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile

98

B



110	115	120
Cys 125	Pro Asp Gly Phe Phe Ser 130	Asn Glu Thr Ser Ser 135
Arg 140	Lys His Thr Asn Cys 145	Ser Val Phe Gly Leu 150
Gly Asn Ala Thr His 160	Asp Asn Ile Cys Ser 165	Gly Asn Ser Glu Ser 170
Gln Lys Cys Gly 175	Ile Asp Ile Asp Leu 180	Cys Glu Asn Ser Val 185
His Ile Gly 190	His Ala Asn Leu Thr 195	Phe Glu Gln Leu Arg 200
Glu Ser 205	Leu Pro Gly Lys Lys 210	Val Gly Ala Glu Asp 215
Ile Lys Ala Cys Lys 220	Pro Ser Asp Gln Ile Leu 230	Lys Leu Leu Ser Leu 235
Trp Arg Ile Lys 240	Asn Gly Asp Gln Asp Thr 245	Leu Lys Gly Leu Met 250
Ala Leu Lys 255	His Ser Lys Thr Tyr His 260	Phe Pro Lys Thr Val 265
Ser Leu Lys 270	Lys Thr Ile Arg Phe 275	Leu His Ser Phe Thr 280
Leu Tyr 285	Gln Lys Leu Phe Leu 290	Glu Met Ile Gly Asn 295
Val Lys Ile Ser Cys 300	Leu 305	

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 327 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..306
  - (D) OTHER INFORMATION: /note= "OCIF-DDD2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
 

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20					-15						-10				
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1				5					10		
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15					20				25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
			30				35					40			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
45						50					55				
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu

60					65					70				75	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
				80					85					90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
			95					100					105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
			110				115					120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
	125					130					135				
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
140					145					150					155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr
				160					165					170	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg
			175					180					185		
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val
		190					195					200			
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
	205					210					215				
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu
220					225					230					235
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln
				240					245					250	
Asp	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr
			255					260					265		
Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr
		270					275					280			
Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln
	285					290					295				
Ser	Val	Lys	Ile	Ser	Cys	Leu									
300					305										

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 399 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0

- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..378
  - (D) OTHER INFORMATION: /note= "OCIF-CL"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
	-20				-15						-10				
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1				5						10	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr



(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..330  
 (D) OTHER INFORMATION: /note= "OCIF-CC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15						-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
		30					35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
	45					50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70					75		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85					90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100					105			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
		110					115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	
				160					165					170		
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	
			175					180					185			
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	
		190					195					200				
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	
	205					210					215					
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	
220					225					230					235	
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	
				240					245					250		
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	
			255					260					265			
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	
		270					275					280				
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	
	285					290					295					
Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	
300					305					310					315	





(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: /note= "OCIF-CDD1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
160 165 170

Gln Lys Cys Gly Ile  
175

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: /note= "OCIF-CCR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10  
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10  
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25  
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40  
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55  
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75  
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90  
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105  
Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys  
110 115 120

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: /note= "OCIF-CCR3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10  
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10  
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25  
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40  
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55  
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu  
80 85

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: /note= "OCIF-CBst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile		
-20					-15						-10						
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp		
-5				1				5					10				
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr		
			15					20					25				
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro		
		30					35					40					
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys		
	45					50					55						
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu		
60					65				70					75			
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr		
				80					85					90			
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe		
			95					100					105				
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg		
			110				115					120					
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys		
	125					130					135						
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys		
140					145					150					155		
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr		
				160					165					170			
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg		
			175					180					185				
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val		
		190					195					200					
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile		
	205					210					215						
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu		
220					225					230					235		
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln		
				240					245					250			

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Leu Val  
 365 370

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /note= "OCIF-CSph"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120  
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135

108

b

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Ser Leu  
 285 290 295  
 Asp  
 300

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: /note= "OCIF-CBsp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55  
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
                     95                                    100                                    105  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
                     110                                    115                                    120  
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
                     125                                    130                                    135  
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
                     140                                    145                                    150                                    155  
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly  
                                     160                                    165

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..63
  - (D) OTHER INFORMATION: /note= "OCIF-CPst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
      -20                                    -15                                    -10  
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
      -5                                    1                                    5                                    10  
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
                     15                                    20                                    25  
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
                     30                                    35                                    40  
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
                     45                                    50                                    55  
 Leu Tyr Leu Val  
      60

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1206
  - (D) OTHER INFORMATION: /note= "(OCIF-C19S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC

60

110

B

CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AAAGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTTCTACAA	AGTTTACGCC	TAAGTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCCAAACT	1080
GTCCTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
TTATAA						1206

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C20S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540



CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGAGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT	1080
GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC	1200
TTATAA	1206

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C21S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCGCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCAG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020

ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080  
 GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140  
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200  
 TTATAA 1206

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C22S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420  
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600  
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTTACAA AGTTTACGCC TAACTGGCTT 660  
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720  
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780  
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840  
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900  
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAAGCAAA 960  
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020  
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080  
 GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140  
 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200  
 TTATAA 1206

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C23S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG      120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC      180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT      240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC      300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA      360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA      420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT      480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA      540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC      600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTTACAA AGTTTACGCC TAACTGGCTT      660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA      720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA      780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC      840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA      900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA      960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC     1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT     1080
GTCACCTAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG     1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCAGC     1200
TTATAA                                           1206
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1083
- (D) OTHER INFORMATION: /note= "(OCIF-DCR1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAACCTT GCCCTGACCA CTACTACACA GACAGCTGGC ACACCAGTGA CGAGTGTCTA      120
TACTGCAGCC CCGTGTGCAA GGAGCTGCAG TACGTCAAGC AGGAGTGCAA TCGCACCCAC      180
```

AACCGCGTGT	GCGAATGCAA	GGAAGGGCGC	TACCTTGAGA	TAGAGTTCTG	CTTGAAACAT	240
AGGAGCTGCC	CTCCTGGATT	TGGAGTGGTG	CAAGCTGGAA	CCCCAGAGCG	AAATACAGTT	300
TGCAAAAGAT	GTCCAGATGG	GTTCTTCTCA	AATGAGACGT	CATCTAAAGC	ACCCTGTAGA	360
AAACACACAA	ATTGCAGTGT	CTTTGGTCTC	CTGCTAACTC	AGAAAGGAAA	TGCAACACAC	420
GACAACATAT	GTTCCGGAAG	CAGTGAATCA	ACTCAAAAAT	GTGGAATAGA	TGTTACCCTG	480
TGTGAGGAGG	CATTCTTCAG	GTTTGCTGTT	CCTACAAAGT	TTACGCCTAA	CTGGCTTAGT	540
GTCTTGGTAG	ACAATTTGCC	TGGCACCAAA	GTAAACGCAG	AGAGTGTAGA	GAGGATAAAA	600
CGGCAACACA	GCTCACAAGA	ACAGACTTTC	CAGCTGCTGA	AGTTATGGAA	ACATCAAAAC	660
AAAGACCAAG	ATATAGTCAA	GAAGATCATC	CAAGATATTG	ACCTCTGTGA	AAACAGCGTG	720
CAGCGGCACA	TTGGACATGC	TAACCTCACC	TTCGAGCAGC	TTCGTAGCTT	GATGGAAAGC	780
TTACCGGGAA	AGAAAGTGGG	AGCAGAAGAC	ATTGAAAAAA	CAATAAAGGC	ATGCAAACCC	840
AGTGACCAGA	TCCTGAAGCT	GCTCAGTTTG	TGGCGAATAA	AAAATGGCGA	CCAAGACACC	900
TTGAAGGGCC	TAATGCACGC	ACTAAAGCAC	TCAAAGACGT	ACCACTTTCC	CAAACTGTG	960
ACTCAGAGTC	TAAAGAAGAC	CATCAGGTTT	CTTCACAGCT	TCACAATGTA	CAAATTGTAT	1020
CAGAAGTTAT	TTTTAGAAAT	GATAGGTAAC	CAGGTCCAAT	CAGTAAAAAT	AAGCTGCTTA	1080
TAA						1083

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1080
- (D) OTHER INFORMATION: /note= "(OCIF-DCR2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCG	AATGCAAGGA	AGGGCGCTAC	CTTGAGATAG	AGTTCTGCTT	GAAACATAGG	240
AGCTGCCCTC	CTGGATTTGG	AGTGGTGCAA	GCTGGAACCC	CAGAGCGAAA	TACAGTTTGC	300
AAAAGATGTC	CAGATGGGTT	CTTCTCAAAT	GAGACGTCAT	CTAAAGCACC	CTGTAGAAAA	360
CACACAAATT	GCAGTGTCTT	TGGTCTCCTG	CTAACTCAGA	AAGGAAATGC	AACACACGAC	420
AACATATGTT	CCGGAAACAG	TGAATCAACT	CAAAAATGTG	GAATAGATGT	TACCCTGTGT	480
GAGGAGGCAT	TCTTCAGGTT	TGCTGTTTCT	ACAAAGTTTA	CGCCTAACTG	GCTTAGTGTC	540
TTGGTAGACA	ATTTGCCTGG	CACCAAAGTA	AACGCAGAGA	GTGTAGAGAG	GATAAAACGG	600
CAACACAGCT	CACAAGAACA	GACTTTCCAG	CTGCTGAAGT	TATGGAAACA	TCAAAACAAA	660
GACCAAGATA	TAGTCAAGAA	GATCATCCAA	GATATTGACC	TCTGTGAAAA	CAGCGTGCAG	720
CGGCACATTG	GACATGCTAA	CCTCACCTTC	GAGCAGCTTC	GTAGCTTGAT	GGAAAGCTTA	780

CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAAACAA TAAAGGCATG CAAACCCAGT	840
GACCAGATCC TGAAGCTGCT CAGTTTGTGG CGAATAAAAA ATGGCGACCA AGACACCTTG	900
AAGGGCCTAA TGCACGCACT AAAGCACTCA AAGACGTACC ACTTTCCCAA AACTGTCACT	960
CAGAGTCTAA AGAAGACCAT CAGGTTCTTT CACAGCTTCA CAATGTACAA ATTGTATCAG	1020
AAGTTATTTT TAGAAATGAT AGGTAACCAG GTCCAATCAG TAAAAATAAG CTGCTTATAA	1080

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1092
- (D) OTHER INFORMATION: /note= "(OCIF-DCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCAGATG TCCAGATGGG TTCTTCTCAA ATGAGACGTC ATCTAAAGCA	360
CCCTGTAGAA AACACACAAA TTGCAGTGTC TTTGGTCTCC TGCTAACTCA GAAAGGAAAT	420
GCAACACACG ACAACATATG TTCCGGAAAC AGTGAATCAA CTCAAAAATG TGGGAATAGAT	480
GTTACCCTGT GTGAGGAGGC ATTCTTCAGG TTTGCTGTTT CTACAAAGTT TACGCCTAAC	540
TGGCTTAGTG TCTTGGTAGA CAATTTGCCT GGCACCAAAG TAAACGCAGA GAGTGTAGAG	600
AGGATAAAAC GGCAACACAG CTCACAAGAA CAGACTTTCC AGCTGCTGAA GTTATGGAAA	660
CATCAAAACA AAGACCAAGA TATAGTCAAG AAGATCATCC AAGATATTGA CCTCTGTGAA	720
AACAGCGTGC AGCGGCACAT TGGACATGCT AACCTCACCT TCGAGCAGCT TCGTAGCTTG	780
ATGGAAAGCT TACCGGGAAA GAAAGTGGGA GCAGAAGACA TTGAAAAAAC AATAAAGGCA	840
TGCAAACCCA GTGACCAGAT CCTGAAGCTG CTCAGTTTGT GGCGAATAAA AAATGGCGAC	900
CAAGACACCT TGAAGGGCCT AATGCACGCA CTAAAGCACT CAAAGACGTA CCACTTTCCC	960
AAAAGTGTCA CTCAGAGTCT AAAGAAGACC ATCAGGTTCC TTCACAGCTT CACAATGTAC	1020
AAATTGTATC AGAAGTTATT TTTAGAAATG ATAGGTAACC AGGTCCAATC AGTAAAAATA	1080
AGCTGCTTAT AA	1092

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1080
- (D) OTHER INFORMATION: /note= "(OCIF-DCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACG	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAAG	GCGAAATACA	420
GTTTGCAAAT	CCGGAAACAG	TGAATCAACT	CAAAAATGTG	GAATAGATGT	TACCCTGTGT	480
GAGGAGGCAT	TCTTCAGGTT	TGCTGTTCTT	ACAAAGTTTA	CGCCTAACTG	GCTTAGTGTC	540
TTGGTAGACA	ATTTGCCTGG	CACCAAAGTA	AACGCAGAGA	GTGTAGAGAG	GATAAACCGG	600
CAACACAGCT	CACAAGAACA	GACTTTCCAG	CTGCTGAAGT	TATGGAAACA	TCAAAACAAA	660
GACCAAGATA	TAGTCAAGAA	GATCATCCAA	GATATTGACC	TCTGTGAAAA	CAGCGTGCAG	720
CGGCACATTG	GACATGCTAA	CCTCACCTTC	GAGCAGCTTC	GTAGCTTGAT	GGAAAGCTTA	780
CCGGGAAAGA	AAGTGGGAGC	AGAAGACATT	GAAAAACAA	TAAAGGCATG	CAAACCCAGT	840
GACCAGATCC	TGAAGCTGCT	CAGTTTGTGG	CGAATAAAAA	ATGGCGACCA	AGACACCTTG	900
AAGGGCCTAA	TGCACGCACT	AAAGCACTCA	AAGACGTACC	ACTTTCCCAA	AACTGTCACT	960
CAGAGTCTAA	AGAAGACCAT	CAGGTTTCCT	CACAGCTTCA	CAATGTACAA	ATTGTATCAG	1020
AAGTTATTTT	TAGAAATGAT	AGGTAACCAG	GTCCAATCAG	TAAAAATAAG	CTGCTTATAA	1080

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..981
- (D) OTHER INFORMATION: /note= "(OCIF-DDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACG	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300

CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATATTGAC	600
CTCTGTGAAA	ACAGCGTGCA	GCGGCACATT	GGACATGCTA	ACCTCACCTT	CGAGCAGCTT	660
CGTAGCTTGA	TGGAAAGCTT	ACCGGGAAAG	AAAGTGGGAG	CAGAAGACAT	TGAAAAAACA	720
ATAAAGGCAT	GCAAACCCAG	TGACCAGATC	CTGAAGCTGC	TCAGTTTGTG	GCGAATAAAA	780
AATGGCGACC	AAGACACCTT	GAAGGGCCTA	ATGCACGCAC	TAAAGCACTC	AAAGACGTAC	840
CACTTTCCCA	AAACTGTCAC	TCAGAGTCTA	AAGAAGACCA	TCAGGTTCTT	TCACAGCTTC	900
ACAATGTACA	AATTGTATCA	GAAGTTATTT	TTAGAAATGA	TAGGTAACCA	GGTCCAATCA	960
GTAAAAATAA	GCTGCTTATA	A				981

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 984 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..984
- (D) OTHER INFORMATION: /note= "(OCIF-DDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTTCTACAA	AGTTTACGCC	TAAGTGCTTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGACG	CACTAAAGCA	CTCAAAGACG	840
TACCACTTTC	CCAAAACCTG	CACTCAGAGT	CTAAAGAAGA	CCATCAGGTT	CCTTCACAGC	900
TTCACAATGT	ACAAATTGTA	TCAGAAGTTA	TTTTTAGAAA	TGATAGGTAA	CCAGGTCCAA	960
TCAGTAAAAA	TAAGCTGCTT	ATAA				984

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: /note= "(OCIF-CL)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT	1080
GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTAA	1200

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1056
- (D) OTHER INFORMATION: /note= "(OCIF-CC)"

B



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTTACAA	AGTTTACGCC	TAAGTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTGA			1056

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 819 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..819  
(D) OTHER INFORMATION: /note= "(OCIF-CDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600

CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAATGA	819

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 594 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..594
- (D) OTHER INFORMATION: /note= "(OCIF-CDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT ATGA	594

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: /note= "(OCIF-CCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360

CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420  
GTTTGCAAAT GA 432

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..321  
(D) OTHER INFORMATION: /note= "(OCIF-CCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCGAATG A 321

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1182  
(D) OTHER INFORMATION: /note= "(OCIF-CBst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60  
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120  
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180  
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240  
CTATACTGCA GCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300  
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360  
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420  
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480  
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540  
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600  
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660

AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT	1080
GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCTAGTCT AG	1182

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 966 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..966  
 (D) OTHER INFORMATION: /note= "(OCIF-CSph)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAAG	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTTCTACAA	AGTTTACGCC	TAAGTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCTAGTCTA	960
GACTAG						966

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 564 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..564

(D) OTHER INFORMATION: /note= "(OCIF-CBsp)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG      120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC      180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT      240
CTATACTGCA GCGCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC      300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA      360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA      420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT      480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA      540
CACGACAACA TATGTTCCGG CTAG                                          564
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..255

(D) OTHER INFORMATION: /note= "(OCIF-Pst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG      120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC      180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT      240
CTATACCTAG TCTAG                                          255
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1317 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1317

(D) OTHER INFORMATION: /note= "human OCIF genomic DNA-1"

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1173..1202
- (D) OTHER INFORMATION: /note= "amino acid residues -21 to -12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
CTGGAGACAT ATAAC TTGAA CACTTGGCCC TGATGGGGAA GCAGCTCTGC AGGGACTTTT      60
TCAGCCATCT GTAAACAATT TCAGTGGCAA CCCGCGAACT GTAATCCATG AATGGGACCA      120
CACTTTACAA GTCATCAAGT CTAAC TTCTA GACCAGGGAA TTAATGGGGG AGACAGCGAA      180
CCCTAGAGCA AAGTGCCAAA CTTCTGTCGA TAGCTTGAGG CTAGTGGAAG GACCTCGAGG      240
AGGCTACTCC AGAAGTTCAG CGCGTAGGAA GCTCCGATAC CAATAGCCCT TTGATGATGG      300
TGGGGTTGGT GAAGGGAACA GTGCTCCGCA AGGTTATCCC TGCCCCAGGC AGTCCAATTT      360
TCACTCTGCA GATTCTCTCT GGCTCTAACT ACCCCAGATA ACAAGGAGTG AATGCAGAAT      420
AGCACGGGCT TTAGGGCCAA TCAGACATTA GTTAGAAAAA TTCCTACTAC ATGGTTTATG      480
TAAACTTGAA GATGAATGAT TGCGAACTCC CCGAAAAGGG CTCAGACAAT GCCATGCATA      540
AAGAGGGGCC CTGTAATTTG AGGTTTCAGA ACCCGAAGTG AAGGGGTCAG GCAGCCGGGT      600
ACGGCGGAAA CTCACAGCTT TCGCCCAGCG AGAGGACAAA GGTCTGGGAC ACACTCCAAC      660
TGCGTCCGGA TCTTGGCTGG ATCGGACTCT CAGGGTGGAG GAGACACAAG CACAGCAGCT      720
GCCCAGCGTG TGCCCAGCCC TCCCACCGCT GGTCCCGGCT GCCAGGAGGC TGGCCGCTGG      780
CGGGAAGGGG CCGGGAAACC TCAGAGCCCC GCGGAGACAG CAGCCGCCTT GTTCCTCAGC      840
CCGGTGGCTT TTTTTTCCCC TGCTCTCCCA GGGGACAGAC ACCACCGCCC CACCCCTCAC      900
GCCCCACCTC CCTGGGGGAT CCTTTCCGCC CCAGCCCTGA AAGCGTTAAT CCTGGAGCTT      960
TCTGCACACC CCCCAGCCGC TCCCGCCCAA GCTTCCTAAA AAAGAAAGGT GCAAAGTTTG     1020
GTCCAGGATA GAAAAATGAC TGATCAAAGG CAGGCGATAC TTCCTGTTGC CGGGACGCTA     1080
TATATAACGT GATGAGCGCA CGGGCTGCGG AGACGCACCG GAGCGCTCGC CCAGCCGCCG     1140
CCTCCAAGCC CCTGAGGTTT CCGGGGACCA CAATGAACAA GTTGCTGTGC TGCGCGCTCG     1200
TGGTAAGTCC CTGGGCCAGC CGACGGGTGC CCGGCGCCTG GGGAGGCTGC TGCCACCTGG     1260
TCTCCAACC TCCAGCGGA CCGGCGGGGA AAAAGGCTCC ACTCGCTCCC TCCAAG          1317
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 130..162
- (D) OTHER INFORMATION: /note= "amino acid residues -11 to -1"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(130..162, 163..498, 4503..4694, 6715..6939, 8960..9346)

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: join(163..498, 4503..4694, 6715..6939, 8960..9346)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCTTACTTTG TGCCAAATCT CATTAGGCTT AAGGTAATAC AGGACTTTGA GTCAAATGAT	60
ACTGTTGCAC ATAAGAACAA ACCTATTTTC ATGCTAAGAT GATGCCACTG TGTTCTTTTC	120
TCCTTCTAG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG	168
Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr	
-11 -10 -5 1	
TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG	216
Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu	
5 10 15	
TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA	264
Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr	
20 25 30	
GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA	312
Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr	
35 40 45 50	
GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC	360
Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys	
55 60 65	
AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC	408
Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg	
70 75 80	
GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG	456
Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu	
85 90 95	
AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT	498
Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala	
100 105 110	
GGTACGTGTC AATGTGCAGC AAAATTAATT AGGATCATGC AAAGTCAGAT AGTTGTGACA	558
GTTTAGGAGA AACTTTTGT TCTGATGACA TTATAGGATA GCAAATTGCA AAGGTAATGA	618
AACCTGCCAG GTAGGTACTA TGTGTCTGGA GTGCTTCCAA AGGACCATTG CTCAGAGGAA	678
TACTTTGCCA CTACAGGGCA ATTTAATGAC AAATCTCAAA TGCAGCAAAT TATTCTCTCA	738
TGAGATGCAT GATGGTTTTT TTTTTTTTTT TTAAAGAAAC AAACCTCAAGT TGCATTATTG	798
ATAGTTGATC TATACCTCTA TATTTCACTT CAGCATGGAC ACCTTCAAAC TGCAGCACTT	858
TTTGACAAAC ATCAGAAATG TTAATTTATA CCAAGAGAGT AATTATGCTC ATATTAATGA	918
GA CTCTGGAG TGCTAACAAT AAGCAGTTAT AATTAATTAT GTAAAAAATG AGAATGGTGA	978
GGGGAATTGC ATTTTCATTAT TAAAAACAAG GCTAGTTCTT CCTTTAGCAT GGGAGCTGAG	1038
TGTTTGGGAG GGTAAGGACT ATAGCAGAAT CTCTTCAATG AGCTTATTCT TTATCTTAGA	1098
CAAAACAGAT TGTCAAGCCA AGAGCAAGCA CTTGCCTATA AACCAAGTGC TTTCTCTTTT	1158
GCATTTTGAA CAGCATTGGT CAGGGCTCAT GTGTATTGAA TCTTTTAAAC CAGTAACCCA	1218
CGTTTTTTTT CTGCCACATT TGCGAAGCTT CAGTGCAGCC TATAACTTTT CATAGCTTGA	1278
GAAAATTAAG AGTATCCACT TACTTAGATG GAAGAAGTAA TCAGTATAGA TTCTGATGAC	1338
TCAGTTTGAA GCAGTGTTC TCAACTGAAG CCCTGCTGAT ATTTTAAGAA ATATCTGGAT	1398
TCCTAGGCTG GACTCCTTTT TGTGGGCAGC TGTCTGCGC ATTGTAGAAT TTTGGCAGCA	1458
CCCCTGGACT CTAGCCACTA GATACCAATA GCAGTCCTTC CCCCATGTGA CAGCCAAAAA	1518
TGTCTTCAGA CACTGTCAAA TGTGCGCCAGG TGGCAAAATC ACTCCTGGTT GAGAACAGGG	1578
TCATCAATGC TAAGTATCTG TAACTATTTT AACTCTCAAA ACTTGTGATA TACAAAGTCT	1638

AAATTATTAG	ACGACCAATA	CTTTAGGTTT	AAAGGCATAC	AAATGAAACA	TTCAAAAATC	1698
AAAATCTATT	CTGTTTCTCA	AATAGTGAAT	CTTATAAAAT	TAATCACAGA	AGATGCAAAT	1758
TGCATCAGAG	TCCCTTAAAA	TTCCTCTTCG	TATGAGTATT	TGAGGGAGGA	ATTGGTGATA	1818
GTTCCCTACTT	TCTATTGGAT	GGTACTTTGA	GACTCAAAAG	CTAAGCTAAG	TTGTGTGTGT	1878
GTCAGGGTGC	GGGGTGTGGA	ATCCCATCAG	ATAAAAGCAA	ATCCATGTAA	TTCATTCACT	1938
AAGTTGTATA	TGTAGAAAAA	TGAAAAGTGG	GCTATGCAGC	TTGGAAACTA	GAGAATTTTG	1998
AAAAATAATG	GAAATCACAA	GGATCTTTCT	TAAATAAGTA	AGAAAATCTG	TTTGTAGAAT	2058
GAAGCAAGCA	GGCAGCCAGA	AGACTCAGAA	CAAAAGTACA	CATTTTACTC	TGTGTACACT	2118
GGCAGCACAG	TGGGATTTAT	TTACCTCTCC	CTCCCTAAAA	ACCCACACAG	CGGTTCCCTCT	2178
TGGGAAATAA	GAGGTTTCCA	GCCCAAAGAG	AAGGAAAGAC	TATGTGGTGT	TACTCTAAAA	2238
AGTATTTAAT	AACCGTTTTG	TTGTTGCTGT	TGCTGTTTTG	AAATCAGATT	GTCTCCTCTC	2298
CATATTTTAT	TTACTTCATT	CTGTTAATTC	CTGTGGAATT	ACTTAGAGCA	AGCATGGTGA	2358
ATTCTCAACT	GTAAAGCCAA	ATTTCTCCAT	CATTATAATT	TCACATTTTG	CCTGGCAGGT	2418
TATAATTTTT	ATATTTCCAC	TGATAGTAAT	AAGGTAAAAAT	CATTACTTAG	ATGGATAGAT	2478
CTTTTTCATA	AAAAGTACCA	TCAGTTATAG	AGGGAAGTCA	TGTTTCATGTT	CAGGAAGGTC	2538
ATTAGATAAA	GCTTCTGAAT	ATATTATGAA	ACATTAGTTC	TGTCATTCTT	AGATTCTTTT	2598
TGTTAAATAA	CTTTAAAAGC	TAACCTTACCT	AAAAGAAATA	TCTGACACAT	ATGAACCTCT	2658
CATTAGGATG	CAGGAGAAGA	CCCAAGCCAC	AGATATGTAT	CTGAAGAATG	AACAAGATTC	2718
TTAGGCCCCG	CACGGTGGCT	CACATCTGTA	ATCTCAAGAG	TTTGAGAGGT	CAAGGCGGGC	2778
AGATCACCTG	AGGTCAGGAG	TTCAAGACCA	GCCTGGCCAA	CATGATGAAA	CCCTGCCTCT	2838
ACTAAAAATA	CAAAAATTAG	CAGGGCATGG	TGGTGATGCA	CTGCAACCCT	AGCTACTCAG	2898
GAGGCTGAGA	CAGGAGAATC	TCTTGAACCC	TCGAGGCGGA	GGTTGTGGTG	AGCTGAGATC	2958
CCTCTACTGC	ACTCCAGCCT	GGGTGACAGA	GATGAGACTC	CGTCCCTGCC	GCCGCCCCCG	3018
CCTTCCCCCC	CAAAAAGATT	CTTCTTCATG	CAGAACATAC	GGCAGTCAAC	AAAGGGAGAC	3078
CTGGGTCCAG	GTGTCCAAGT	CACTTATTTT	GAGTAAATTA	GCAATGAAAAG	AATGCCATGG	3138
AATCCCTGCC	CAAATACCTC	TGCTTATGAT	ATTGTAGAAT	TTGATATAGA	GTTGTATCCC	3198
ATTTAAGGAG	TAGGATGTAG	TAGGAAAGTA	CTAAAAACAA	ACACACAAAC	AGAAAAACCCT	3258
CTTTGCTTTG	TAAGGTGGTT	CCTAAGATAA	TGTCAGTGCA	ATGCTGGAAA	TAATATTTAA	3318
TATGTGAAGG	TTTTAGGCTG	TGTTTTCCCC	TCCTGTTCTT	TTTTTCTGCC	AGCCCTTTGT	3378
CATTTTTGCA	GGTCAATGAA	TCATGTAGAA	AGAGACAGGA	GATGAAACTA	GAACCAGTCC	3438
ATTTTGCCCC	TTTTTTTATT	TTCTGGTTTT	GGTAAAAGAT	ACAATGAGGT	AGGAGGTTGA	3498
GATTTATAAA	TGAAGTTTAA	TAAGTTTCTG	TAGCTTTGAT	TTTTCTCTTT	CATATTTGTT	3558
ATCTTGATA	AGCCAGAATT	GGCCTGTAAA	ATCTACATAT	GGATATTGAA	GTCTAAATCT	3618
GTTCAACTAG	CTTACACTAG	ATGGAGATAT	TTTCATATTC	AGATACACTG	GAATGTATGA	3678
TCTAGCCATG	CGTAATATAG	TCAAGTGTTT	GAAGGTATTT	ATTTTTAATA	GCGTCTTTAG	3738
TTGTGGACTG	GTTCAAGTTT	TTCTGCCAAT	GATTTCTTCA	AATTTATCAA	ATATTTTTC	3798
ATCATGAAGT	AAAATGCCCT	TGCAGTCACC	CTTCCTGAAG	TTTGAACGAC	TCTGCTGTTT	3858
TAAACAGTTT	AAGCAAATGG	TATATCATCT	TCCGTTTACT	ATGTAGCTTA	ACTGCAGGCT	3918



TACGCTTTTG AGTCAGCGGC CAACTTTATT GCCACCTTCA AAAGTTTATT ATAATGTTGT	3978
AAATTTTAC TTCTCAAGGT TAGCATACTT AGGAGTTGCT TCACAATTAG GATTCAGGAA	4038
AGAAAGAACT TCAGTAGGAA CTGATTGGAA TTTAATGATG CAGCATTCAA TGGGTACTAA	4098
TTTCAAAGAA TGATATTACA GCAGACACAC AGCAGTTATC TTGATTTTCT AGGAATAATT	4158
GTATGAAGAA TATGGCTGAC AACACGGCCT TACTGCCACT CAGCGGAGGC TGGACTAATG	4218
AACACCCTAC CCTTCTTTCC TTTCTCTCA CATTTTCATGA GCGTTTTGTA GGTAACGAGA	4278
AAATTGACTT GCATTTGCAT TACAAGGAGG AGAACTGGC AAAGGGGATG ATGGTGGAAG	4338
TTTTGTTCTG TCTAATGAAG TGAAAAATGA AAATGCTAGA GTTTTGTGCA ACATAATAGT	4398
AGCAGTAAAA ACCAAGTGAA AAGTCTTTCC AAACTGTGT TAAGAGGGCA TCTGCTGGGA	4458
AACGATTTGA GGAGAAGGTA CTAAATTGCT TGGTATTTTC CGTA GGA ACC CCA GAG	4514
	Gly Thr Pro Glu 115
CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT GGG TTC TTC TCA AAT GAG	4562
Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu	
	120 125 130
ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC ACA AAT TGC AGT GTC TTT	4610
Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe	
	135 140 145
GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA ACA CAC GAC AAC ATA TGT	4658
Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys	
	150 155 160
TCC GGA AAC AGT GAA TCA ACT CAA AAA TGT GGA ATA GGTAATTACA	4704
Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile	
	165 170 175
TTCCAAAATA CGTCTTTGTA CGATTTTGTA GTATCATCTC TCTCTCTGAG TTGAACACAA	4764
GGCCTCCAGC CACATTCTTG GTCAAACCTTA CATTTTCCCT TTCTTGAATC TTAACCAGCT	4824
AAGGCTACTC TCGATGCATT ACTGCTAAAG CTACCACTCA GAATCTCTCA AAAACTCATC	4884
TTCTCACAGA TAACACCTCA AAGCTTGATT TTCTCTCCTT TCACACTGAA ATCAAATCTT	4944
GGCCATAGGC AAAGGGCAGT GTCAAGTTTG CCACTGAGAT GAAATTAGGA GAGTCCAAAC	5004
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GGCTTACTCC TATAATCCCA ACATTTTGGG GGGCCAAGGT AGGCAGATCA CTTGAGGTCA	5184
GGATTTCAAG ACCAGCCTGA CCAACATGGT GAAACCTTGT CTCTACTAAA AATACAAAAA	5244
TTAGCTGGGC ATGGTAGCAG GCACTTCTAG TACCAGCTAC TCAGGGCTGA GGCAGGAGAA	5304
TCGCTTGAAC CCAGGAGATG GAGGTTGCAG TGAGCTGAGA TTGTACCACT GCACTCCAGT	5364
CTGGGCAACA GAGCAAGATT TCATCACACA CACACACACA CACACACACA CACACATTAG	5424
AAATGTGTAC TTGGCTTTGT TACCTATGGT ATTAGTGCAT CTATTGCATG GAACTTCCAA	5484
GCTACTCTGG TTGTGTTAAG CTCTTCATTG GGTACAGGTC ACTAGTATTA AGTTCAGGTT	5544
ATTCGGATGC ATTCCACGGT AGTGATGACA ATTCATCAGG CTAGTGTGTG TGTTACCTT	5604
GTCACCTCCA CCACTAGACT AATCTCAGAC CTTCACTCAA AGACACATTA CACTAAAGAT	5664
GATTTGCTTT TTTGTGTTTA ATCAAGCAAT GGTATAAACC AGCTTGACTC TCCCCAAACA	5724
GTTCCTCGTA CTACAAAGAA GTTTATGAAG CAGAGAAATG TGAATTGATA TATATATGAG	5784
ATTCTAACCC AGTTCCAGCA TTGTTTCATT GTGTAATTGA AATCATAGAC AAGCCATTTT	5844
AGCCTTTGCT TTCTTATCTA AAAAAAAAAA AAAAAAATG AAGGAAGGGG TATTTAAAGG	5904

AGTGATCAAA TTTTAACATT CTCTTTAATT AATTCATTTT TAATTTTACT TTTTTCATT	5964
TATTGTGCAC TTACTATGTG GTACTGTGCT ATAGAGGCTT TAACATTTAT AAAAACACTG	6024
TGAAAGTTGC TTCAGATGAA TATAGGTAGT AGAACGGCAG AACTAGTATT CAAAGCCAGG	6084
TCTGATGAAT CCAAAAACAA ACACCCATTA CTCCCATTTT CTGGGACATA CTTACTCTAC	6144
CCAGATGCTC TGGGCTTTGT AATGCCTATG TAAATAACAT AGTTTTATGT TTGGTTATTT	6204
TCCTATGTAA TGTCTACTTA TATATCTGTA TCTATCTCTT GCTTTGTTTC CAAAGGTAAA	6264
CTATGTGTCT AAATGTGGGC AAAAAATAAC ACACTATTCC AAATTACTGT TCAAATTCCT	6324
TTAAGTCAGT GATAATTATT TGTTTTGACA TTAATCATGA AGTTCCTGT GGGTACTAGG	6384
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TTTACAACAA TATTTCACTC TAATTAGACA TTTACTAAAC TTTCTCTTGA AAACAATGCC	6504
CAAAAAAGAA CATTAGAAGA CACGTAAGCT CAGTTGGTCT CTGCCACTAA GACCAGCCAA	6564
CAGAAGCTTG ATTTTATTCA AACTTTGCAT TTTAGCATAT TTTATCTTGG AAAATTCAAT	6624
TGTGTTGGTT TTTTGTTTTT GTTTGTATTG AATAGACTCT CAGAAATCCA ATTGTTGAGT	6684
AAATCTTCTG GGTTTTCTAA CCTTTCTTTA GAT GTT ACC CTG TGT GAG GAG GCA	6738
Asp Val Thr Leu Cys Glu Glu Ala	180
TTC TTC AGG TTT GCT GTT CCT ACA AAG TTT ACG CCT AAC TGG CTT AGT	6786
Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser	185 190 195 200
GTC TTG GTA GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA	6834
Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val	205 210 215
GAG AGG ATA AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG	6882
Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu	220 225 230
CTG AAG TTA TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG	6930
Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys	235 240 245
ATC ATC CAA GGTAATTACA TTCCAAAATA CGTCTTTGTA CGATTTTGTA	6979
Ile Ile Gln	250
GTATCATCTC TCTCTCTGAG TTGAACACAA GGCCTCCAGC CACATTCTTG GTCAAACTTA	7039
CATTTTCCCT TTCTTGAATC TTAACCAGCT AAGGCTACTC TCGATGCATT ACTGCTAAAG	7099
CTACCACTCA GAATCTCTCA AAAACTCATC TTCTCACAGA TAACACCTCA AAGCTTGATT	7159
TTCTCTCCTT TCACACTGAA ATCAAATCTT GCCCATAGGC AAAGGGCAGT GTCAAGTTTG	7219
CCACTGAGAT GAAATTAGGA GAGTCCAAAC TGTAGAATTC ACGTTGTGTG TTATTACTTT	7279
CACGAATGTC TGTATTATTA ACTAAAGTAT ATATTGGCAA CTAAGAAGCA AAGTGATATA	7339
AACATGATGA CAAATTAGGC CAGGCATGGT GGCTTACTCC TATAATCCCA ACATTTTGGG	7399
GGGCCAAGGT AGGCAGATCA CTTGAGGTCA GGATTTCAAG ACCAGCCTGA CCAACATGGT	7459
GAAACCTTGT CTCTACTAAA AATACAAAAA TTAGCTGGGC ATGGTAGCAG GCACTTCTAG	7519
TACCAGCTAC TCAGGGCTGA GGCAGGAGAA TCGCTTGAAC CCAGGAGATG GAGGTTGCAG	7579
TGAGCTGAGA TTGTACCACT GCACTCCAGT CTGGGCAACA GAGCAAGATT TCATCACACA	7639
CACACACACA CACACACACA CACACATTAG AAATGTGTAC TTGGCTTTGT TACCTATGGT	7699
ATTAGTGCAT CTATTGCATG GAACTTCCAA GCTACTCTGG TTGTGTTAAG CTCTTCATTG	7759

GGTACAGGTC	ACTAGTATTA	AGTTCAGGTT	ATTTCGGATGC	ATTCCACGGT	AGTGATGACA	7819
ATTCATCAGG	CTAGTGTGTG	TGTTACACCTT	GTCACCTCCA	CCACTAGACT	AATCTCAGAC	7879
CTTCACTCAA	AGACACATTA	CACTAAAGAT	GATTTGCTTT	TTTGTGTTTA	ATCAAGCAAT	7939
GGTATAAACC	AGCTTGACTC	TCCCCAAACA	GTTTTTCGTA	CTACAAAGAA	GTTTATGAAG	7999
CAGAGAAATG	TGAATTGATA	TATATATGAG	ATTCTAACCC	AGTTCCAGCA	TTGTTTCATT	8059
GTGTAATTGA	AATCATAGAC	AAGCCATTTT	AGCCTTTGCT	TTCTTATCTA	AAAAAAAAAA	8119
AAAAAAAAATG	AAGGAAGGGG	TATTAAAAGG	AGTGATCAAA	TTTTAACATT	CTCTTTAATT	8179
AATTCATTTT	TAATTTTACT	TTTTTTCATT	TATTGTGCAC	TTACTATGTG	GTAATGTGCT	8239
ATAGAGGCTT	TAACATTTAT	AAAAACACTG	TGAAAGTTGC	TTTTCAGATGAA	TATAGGTAGT	8299
AGAACGGCAG	AACTAGTATT	CAAAGCCAGG	TCTGATGAAT	CCAAAAACAA	ACACCCATTA	8359
CTCCCATTTT	CTGGGACATA	CTTACTCTAC	CCAGATGCTC	TGGGCTTTGT	AATGCCTATG	8419
TAAATAACAT	AGTTTTATGT	TTGGTTATTT	TCCTATGTAA	TGTCTACTTA	TATATCTGTA	8479
TCTATCTCTT	GCTTTGTTTC	CAAAGGTAAA	CTATGTGTCT	AAATGTGGGC	AAAAATAAC	8539
ACACTATTCC	AAATTACTGT	TCAAATTCCT	TTAAGTCAGT	GATAATTATT	TGTTTTGACA	8599
TTAATCATGA	AGTTCCCTGT	GGGTACTAGG	TAAACCTTTA	ATAGAATGTT	AATGTTTGTA	8659
TTCATTATAA	GAATTTTTGG	CTGTTACTTA	TTTACAACAA	TATTTCACTC	TAATTAGACA	8719
TTTACTAAAC	TTTCTCTTGA	AAACAATGCC	CAAAAAAGAA	CATTAGAAGA	CACGTAAGCT	8779
CAGTTGGTCT	CTGCCACTAA	GACCAGCCAA	CAGAAGCTTG	ATTTTATTCA	AACTTTGCAT	8839
TTTAGCATAT	TTTATCTTGG	AAAATTCAAT	TGTGTTGGTT	TTTTGTTTTT	GTTTGTATTG	8899
AATAGACTCT	CAGAAATCCA	ATTGTTGAGT	AAATCTTCTG	GGTTTTCTAA	CCTTTCTTTA	8959
GAT ATT GAC CTC TGT GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT	Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala	255	260	265	9007	
AAC CTC ACC TTC GAG CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA	Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly	270	275	280	9055	
AAG AAA GTG GGA GCA GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA	Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys	285	290	295	9103	
CCC AGT GAC CAG ATC CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT	Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn	300	305	310	315	
GGC GAC CAA GAC ACC TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA	Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser	320	325	330	9199	
AAG ACG TAC CAC TTT CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC	Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr	335	340	345	9247	
ATC AGG TTC CTT CAC AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA	Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu	350	355	360	9295	
TTT TTA GAA ATG ATA GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC	Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys	365	370	375	9343	
TTA TAACTGGAAA TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT	Leu	380	9396			
GGATGAGTAA ACTGTTTCTC AGGCACTTGA GGCTTTTCAGT GATATCTTTC TCATTACCAG			9456			

TGA CTA A T T T T T G C C A C A G G G T A C T A A A A G A A A C T A T G A T G T G G A G A A A G G A C T A A C A T C T 9516  
 C C T C C A A T A A A C C C C A A A T G G T T A A T C C A A C T G T C A G A T C T G G A T C G T T A T C T A C T G A C T 9576  
 A T A T T T T C C C T T A T T A C T G C T T G C A G T A A T C A A C T G G A A A T T A A A A A A A A A A A C T A G A 9636  
 C T C C A C T G G G C C T T A C T A A A T A T G G G A A T G T C T A A C T T A A A T A G C T T T G G G A T T C C A G C T 9696  
 A T G C T A G A G G C T T T T A T T A G A A A G C C A T A T T T T T T T C T G T A A A A G T T A C T A A T A T A T C T G 9756  
 T A A C A C T A T T A C A G T A T T G C T A T T T A T A T T C A T T C A G A T A T A A G A T T T G G A C A T A T T A T C 9816  
 A T C C T A T A A A G A A C G G T A T G A C T T A A T T T T A G A A A G A A A A T T A T A T T C T G T T T A T T A T G 9876  
 A C A A A T G A A A G A G A A A A T A T A T A T T T T A A T G G A A A G T T T G T A G C A T T T T T C T A A T A G G T 9936  
 A C T G C C A T A T T T T T C T G T G T G G A G A T T T T T A T A A T T T T A T C T G T A T A A G C T G T A A T A T C 9996  
 A T T T T A T A G A A A A T G C A T T A T T A G T C A A T T G T T T A A T G T T G G A A A C A T A T G A A A T A T A 10056  
 A A T T A T C T G A A T A T T A G A T G C T C T G A G A A A T T G A A T G T A C C T T A T T T A A A A G A T T T T A T G 10116  
 G T T T T A T A A C T A T A T A A A T G A C A T T A T T A A A G T T T T C A A A T T A T T T T T T A T T G C T T T C T C 10176  
 T G T T G C T T T T A T T T 10190

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro  
 -11 -10 -5 1 5  
 Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp  
 10 15 20  
 Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp  
 25 30 35  
 Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp  
 40 45 50  
 His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu  
 55 60 65  
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu  
 70 75 80 85  
 Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg  
 90 95 100  
 Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg  
 105 110 115  
 Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr  
 120 125 130  
 Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly  
 135 140 145  
 Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser  
 150 155 160 165  
 Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys  
 170 175 180  
 Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn  
 185 190 195

Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala  
 200 205 210  
 Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr  
 215 220 225  
 Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile  
 230 235 240 245  
 Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln  
 250 255 260  
 Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu  
 265 270 275  
 Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys  
 280 285 290  
 Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser  
 295 300 305  
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met  
 310 315 320 325  
 His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr  
 330 335 340  
 Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr  
 345 350 355  
 Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln  
 360 365 370  
 Ser Val Lys Ile Ser Cys Leu  
 375 380

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer 2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CARGARCARA CNTTYCARYT

20

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer 3R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

YTTTACATN GTRAANSWRT G

21

132

b